Sequencing depth	% Obs. 5hmC	P-value	Number reading as C in BS-Seq	Number reading as C in oxBS-Seq
20	35%	0.0098 **	19	12
	25%	0.0457 *		14
50	18%	0.0073 **	48	39
	12%	0.0458 *		42
100	11%	0.0096 **	95	84
	8%	0.0407 *		87
500	4%	0.0090 **	475	455
	3%	0.0462 *		461

Fisher's test of varying sequence coverage. P-values obtained from Fisher's exact test to the null hypothesis that the proportion of methylated reads in BS-Seq is equal to that of oxBS-Seq (alternative hypothesis: methylated read count in BS-Seq > oxBS-Seq). Four scenarios of sequencing depth are shown, where the level of 5mC and 5hmC in BS-Seq is fixed at 95% for a single base position. Two p-values are given for each sequencing depth, along with two observed levels of 5hmC and hence number reading as C in oxBS-Seq. For example, at a sequencing depth of 50, when 48 of these reads are C in BS-Seq and 39 reads are C in oxBS-Seq, the difference is 9 reads. 9 reads out of 50 gives 18% 5hmC, which gives a p-value of 0.0073.

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